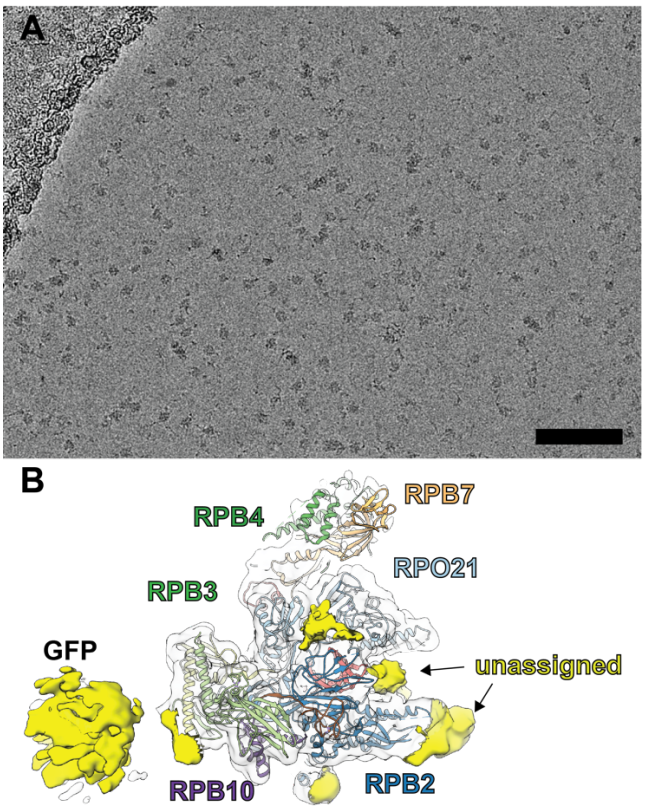


Figure 1. A. raw cryo-EM micrograph taken on an Arctica/K3 of natively purified RNA polymerase II B. a preliminary 5.2 Å reconstruction with the docked crystal structure of RNA pol II. Highlighted in yellow are the unassigned densities, possibly including additional nucleic acid substrate.

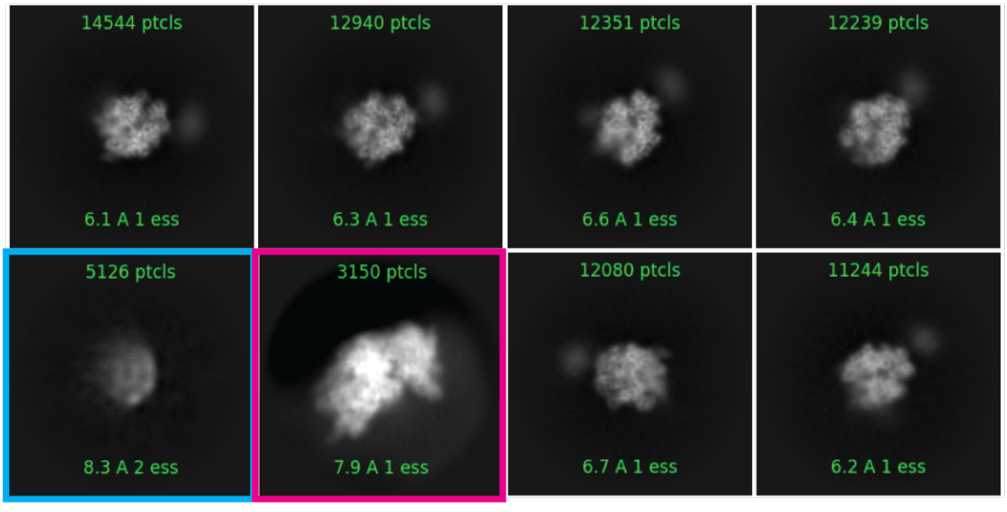


Figure 2. Selected 2D class averages of the natively purified RNA polymerase sample. Highlighted in blue is a 2D class that resembles a nucleosome. Highlighted in pink is an as-yet unidentified ensemble of factors.

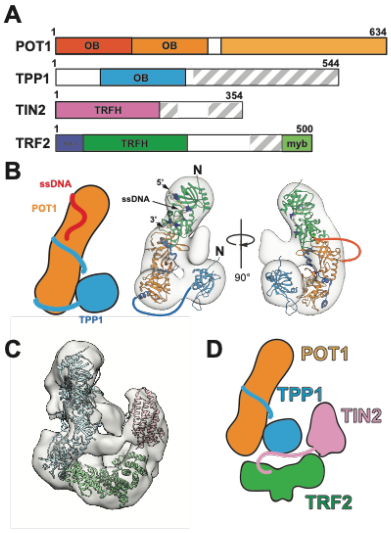
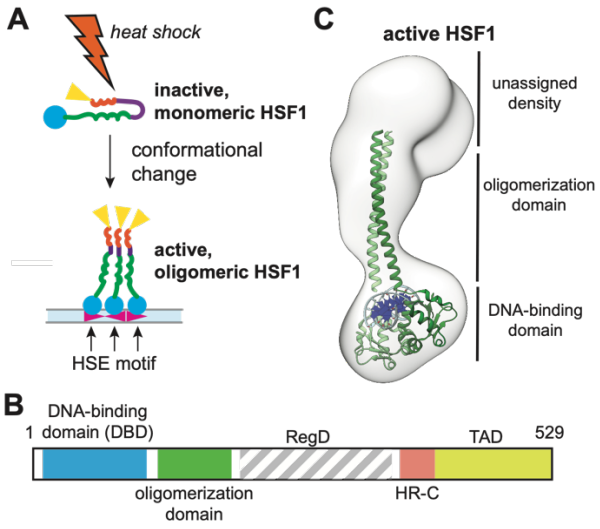
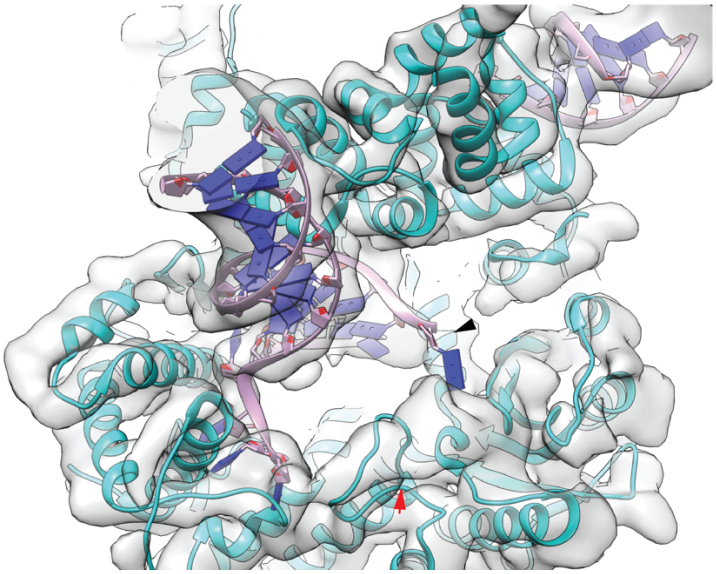


Figure 1 Shelterin preliminary architectural model. A. Functional domains of each component shelterin gene. Colored boxes indicate solved crystal structure, gray shaded indicate regions of flexibility. B. Architecture of shelterin sub-complex: TPP1-POT1, which binds ssDNA. C. preliminary cryo-EM structure of full shelterin complex. D. modeled architecture of full shelterin complex (no DNA)



Preliminary structure of HSF1. A. HSF1 undergoes a structural rearrangement when activated by heat. B. Diagram of the functional domains of HSF1. C. Preliminary structure of activated full-length HSF1. Existing crystal structures fit within the density, and remaining density for the activation domains remains unassigned.



Preliminary 4.5 Å reconstruction of the cleaved-donor complex P element transposase. In the absence of GTP, this structure reveals additional density (red arrow) as well as missing density for both nucleotide as well as the terminal inverted repeat (black arrow) indicating that likely there are structural rearrangements that would be visualized at higher resolution.